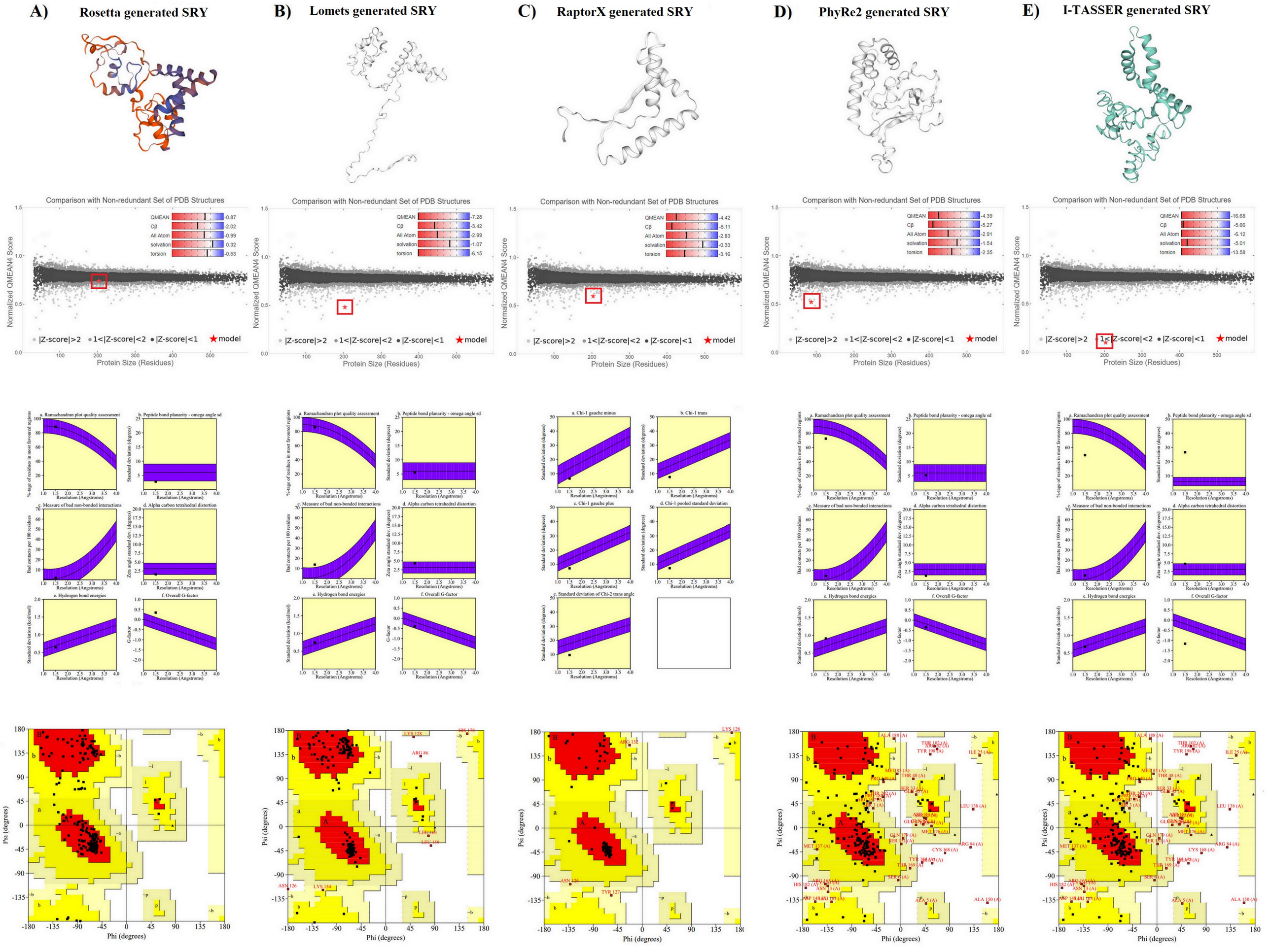

Supplementary Figure 1. Comparison between the efficiency of A) Rosetta, B) LOMETS, C) RaptorX, D) PhyRe2, and E) I-TASSER in generating 3-dimensional structure of SRY protein. The parameters used in comparisons are normalization QMEAN values, side chains, and psi/phi parameters of Ramachandran plots in the PROCHECK tool.

Research title. The highly deleterious F109S mutation can disrupt the binding of sex-determining region Y protein with DNA; an in silico approach

Journal name. Karbala International Journal of Modern Science

Authors names and affiliations. Mohammed Baqur S. Al-Shuhaib[1]*, Sayed AbdulAzeez[2], J. Francis Borgio[3]

[1]Department of Animal Production, College of Agriculture, Al-Qasim Green University, Al-Qasim, Babil 51001, Iraq
[2]Department of Genetic Research, Institute for Research and Medical Consultations (IRMC), Imam Abdulrahman Bin Faisal University, Dammam, Saudi Arabia
[3]Department of Genetic Research, Institute for Research and Medical Consultations (IRMC), Imam Abdulrahman Bin Faisal University, Dammam, Saudi Arabia

E-mail addresses of the corresponding author: baquralhilly_79@yahoo.com; mohammed79@agre.uoqasim.edu.iq